COMPLETE LISTING OF ALL CLAIMS IN THE APPLICATION

1.(currently amended) A peptide fragment having the general sequence

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys (SEQ ID NO:1),

where the variables X^1 to X^6 in the sequence have the following meanings:

X^1 = an amino acid selected from the group consisting of Ala, Val, Phe, Ser, Met,

Trp, Tyr, Asn, Asp or Lys and the variables X^2 to X^6 an amino acid

selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser,

Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^2 = an amino acid selected from the group consisting of Val, Ile, Phe, Pro, Trp,

Tyr, Gln, Glu or Arg and the variables X^1, X^3 to X^6 an amino acid selected

from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr,

Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^3 = an amino acid selected from the group consisting of Gly, Ile, Thr, Met, Trp,

Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and the variables X^1, X^2, X^4 to X^6 an

amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile,

Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^4 = an amino acid selected from the group consisting of Val, Phe, Pro, Cys, Met,

Trp, Asn, Glu, Arg or His and the variables X^1 to X^3, $X^{5,}$ X^6 an amino acid

selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser,

Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^5 = an amino acid selected from the group consisting of Gly, Ser, Cys, Met, Trp,

Asn, Glu, Lys or Arg and the variables X^1 to X^4, X^6 an amino acid selected

from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr,

Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^6 = an amino acid selected from the group consisting of Phe, Pro, Ser, Cys, Trp,

Tyr or Gln and the variables X^1 to X^5 an amino acid selected from the

group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met,

Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and

where at least one of the variables X^1 to X^6 in the sequence is, independently of

one another, Gln or Asn.

2. (original) A peptide fragment as claimed in claim 1, in which the variables X^1 to X^6

have the meanings stated in claim 1, where at least one of the variables X^1 to X^6

in the sequence is, independently of one another, Lys or Arg.

3. (previously amended) A peptide fragment as claimed in claim 1, in which the

variables X^1 to X^6 in the sequence have the following meanings independently of

one another:

X^1 = an amino acid selected from the group consisting of Ala, Val, Phe, Ser, Met,

Trp, Tyr, Asn, Asp or Lys;

X^2 = an amino acid selected from the group consisting of Val, Ile, Phe, Pro, Trp,

Tyr, Gln, Glu or Arg;

X^3 = an amino acid selected from the group consisting of Gly, Ile, Thr, Met, Trp,

Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His;

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X^4 = an amino acid selected from the group consisting of Val, Phe, Pro, Cys, Met,

Trp, Asn, Glu, Arg or His;

X^5 = an amino acid selected from the group consisting of Gly, Ser, Cys, Met, Trp,

Asn, Glu, Lys or Arg;

X^6 = an amino acid selected from the group consisting of Phe, Pro, Ser, Cys, Trp,

Tyr or Gln.

4.(previously amended) A peptide fragment as claimed in claim 1, in which the

variables X^1 to X^6 in the sequence have the following meanings independently of

one another:

X^1 = an amino acid selected from the group consisting of Phe, Ser, Asn, Asp or

Lys;

X^2 = an amino acid selected from the group consisting of Val, Ile, Phe, Pro, Gln,

Glu or Arg;

X^3 = an amino acid selected from the group consisting of Gly, Ile, Thr, Met, Trp,

Tyr, Asn, Asp, Glu, Arg or His;

X^4 = an amino acid selected from the group consisting of Val, Phe, Cys, Met, Trp,

Asn, Arg or His;

X^5 = an amino acid selected from the group consisting of Gly, Ser, Cys, Met, Asn,

Glu, Lys or Arg;

X^6 = an amino acid selected from the group consisting of Phe, Ser, Cys, or Tyr.

5. (previously amended) A peptide fragment as claimed in claim 1 , in which the

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variables X^1 to X^6 in the sequence have the following meanings:

X^1 = Asn;

X^2 = Gln, Glu or Arg;

X^3 = Gly, Thr or Tyr;

X^4 = Asn or Arg;

X^5 = Gly or Lys;

X^6 = Cys.

6. (currently amended) A peptide fragment having the sequence

   His-Gln-His-Glu-Gly-Arg-Cys-Lys-Glu-Cys (SEQ ID NO:2)

   His-Asn-His-Arg-Tyr-Gly-Cys-Gly-Cys-Cys (SEQ ID NO:3)

   His-Arg-His-Gly-Thr-Asn-Cys-Leu-Lys-Cys (SEQ ID NO:4)

   His-Ile-His-Gln-Ser-Asn-Cys-Gln-Val-Cys (SEQ ID NO:5).

7. (withdrawn) A fusion protein comprising a protein fragment as claimed claim 1.

8. (withdrawn) A nucleic acid fragment coding for a protein fragment as claimed in claim

   1.

9. (withdrawn) A nucleic acid comprising a nucleic acid fragment as claimed in claim 8.

10. (withdrawn) A nucleic acid coding for a fusion protein as claimed in claim 7.

11. (withdrawn) A vector comprising a nucleic acid fragment as claimed in claim 8.

12. (withdrawn) A process for preparing fusion proteins as claimed in claim 7, which

   comprises fusing a nucleic acid fragment to a gene which codes for a protein.

13. (withdrawn) A process for purifying fusion proteins as claimed in claim 7, which

comprises

a)   bringing liquids which contain the fusion protein into contact with

immobilized metal ions in such a way that an affinity linkage can form

between the metal ions and the fusion protein,

b)   removing unbound substances present in the liquid,

c)   eluting the bound fusion protein by abolishing the affinity linkage by

changing the liquid medium and

d)   collecting the purified fusion protein.

14. (withdrawn) The use of a protein fragment as claimed in claim 1 or of a nucleic acid

fragment for purifying proteins.

15. (currently amended/withdrawn) A process for preparing protein fragments able to

enter into a reversible affinity linkage with immobilized metal ions, which

comprises carrying out the following steps:

a)   preparing a nucleic acid library starting from any suitable nucleic acid

sequence which codes for a protein fragment of the sequence

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys (SEQ ID NO:11),

where the histidine and cysteine residues of the sequence are conserved

in the nucleic acid library,

b)   fusing the nucleic acids of the library to a reporter gene which makes it

possible to detect the fusion protein encoded by the resulting nucleic acid

via its binding to the immobilized metal ions and

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c)   selecting the nucleic acid sequences which display a reversible binding to the immobilized metal ions which is at least 1.5 times stronger than the sequence in the natural Helicobacter pylori ATPase-439.

16. (withdrawn) A process as claimed in claim 15, wherein the egf protein from Aequoria victoria is used as reporter gene.

17. (withdrawn) A method for detecting proteins, which comprises detecting individual proteins which comprise a protein fragment as claimed in claim 1 in a protein mixture via antibodies which are directed against the protein fragment.

18. (withdrawn) The use of a protein fragment as claimed in claim 1 of a nucleic acid fragment for purifying proteins.